

SEQUENCE LISTING

<110> Ford, John
Mulero, Julio

<120> METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
POLYPEPTIDES

<130> 28111/35908

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<150> PCT/US99/16180
<151> 1999-07-16

<150> 09/350,836
<151> 1999-07-09

<150> 09/273,447
<151> 1999-03-19

<150> 09/244,444
<151> 1999-02-04

<150> 09/122,449
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<170> PatentIn Ver. 2.0

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tttgagaaaa ctctggaaaca aactcctagg ggctaccta cttcccttga gatgttaac 180
agcaactata agctctatac acatagttac ctgggatttg gattgaaagc tgcaagacta 240
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aaaagtgata taataaagga accaaggaga aaattcagaa ggaaagaaaa aattgcctct 180

gcaggtgtgc gagcaggatt gcttcgtcaa caaaagcctc cacccagcca catcttggga 240

aaaga atg gcc act tct tgg ggc aca gtc ttt ttc atg ctg gtg gta tcc 290

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser

1

5

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tgt gtt tgc agc gct gtc tcc cac agg aac cag cag act tgg ttt gag 338

Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu

20

25

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ggc atc ttc ctg tct tcc atg tgc ccc atc aat gtc agc gcc agc acc 386

Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr

35

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ttg tat gga att atg ttt gat gca ggg agc act gga act cga att cat 434

Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His

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gtt tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta gaa 482

Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu

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70

75

ggc gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta gat 530

Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp

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85

90

95

caa cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg gcc 578

Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala

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105

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aaa gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc cta 626

Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu

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aag gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag gct 674

Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala

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ctg ctc ttt gag gta aag gag atc ttc agg aag tca cct ttc ctg gta 722

Leu Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val

145

150

155

cca aag ggc agt gtt agc atc atg gat gga tcc gac gaa ggc ata tta 770

Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu

160

165

170

175

gct tgg gtt act gtg aat ttt ctg aca ggt cag ctg cat ggc cac aga 818

Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg

180

185

190

cag gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa atc Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile .	195	200	205	866
acg ttc ctg ccc cag ttt gag aaa act ctg gaa caa act cct agg ggc Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly 210	215	220	.	914
tac ctc act tcc ttt gag atg ttt aac agc act tat aag ctc tat aca Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr 225	230	235	.	962
cat agt tac ctg gga ttt gga ttg aaa gct gca aga cta gca acc ctg His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu 240	245	250	255	1010
gga gcc ctg gag aca gaa ggg act gat ggg cac act ttc cg ^g agt gcc Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala 260	265	270	.	1058
tgt tta ccg aga tgg ttg gaa gca gag tgg atc ttt ggg ggt gtg aaa Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys 275	280	285	.	1106
tac cag tat ggt ggc aac caa gaa ggg gag gtg ggc ttt gag ccc tgc Tyr Gln Tyr Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys 290	295	300	.	1154
tat gcc gaa gtg ctg agg gtg gta cga gga aaa ctt cac cag cca gag Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu 305	310	315	.	1202
gag gtc cag aga ggt tcc ttc tat gct ttc tct tac tat tat gac cga Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg 320	325	330	335	1250
gct gtt gac aca gac atg att gat tat gaa aag ggg ggt att tta aaa Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys 340	345	350	.	1298
gtt gaa gat ttt gaa aga aaa gcc agg gaa gtg tgt gat aac ttg gaa Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu 355	360	365	.	1346
aac ttc acc tca ggc agt cct ttc ctg tgc atg gat ctc agc tac atc Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile 370	375	380	.	1394
aca gcc ctg tta aag gat ggc ttt ggc ttt gca gac agc aca gtc tta Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu 385	390	395	.	1442
cag ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg ggg Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly 400	405	410	415	1490
gcc acc ttt cac ctg ttg cag tct ctg ggc atc tcc cat tgaggccacg Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His 420	425	.	.	1539
tacttccttg gagacctgca tttgccaaca ccttttaag gggaggagag agcacttagt	1599	.	.	.

ttctgaacta gtctggggac atcctggact tgagcctaga gattwrgtta attaascggc 1659
cgagcttatac cttwatragg taatttactt gcmtggccgc gtttacacgt cgtgatggna 1719
aacctgcgtc ccaactaacg cttgasamat ccccttcgca gctgcgatac caaaagccga 1779
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Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
35 40 45
Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
50 55 60
Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
65 70 75 80
Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
85 90 95
Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
100 105 110

Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
115 120 125
Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
130 135 140
Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
145 150 155 160
Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
165 170 175
Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
180 185 190
Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
195 200 205
Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
210 215 220
Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
225 230 235 240
Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly

245	250	255
Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys		
260	265	270
Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr		
275	280	285
Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr		
290	295	300
Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu		
305	310	315
Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala		
325	330	335
Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val		
340	345	350
Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn		
355	360	365
Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr		
370	375	380
Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln		
385	390	395
Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala		
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Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His		
420	425	

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gtt tgc agc gct gtc tcc cac agg aac cag cag act tgg ttt gag ggt 96
Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
 20 25 30

atc ttc ctg tct tcc atg tgc ccc atc aat gtc agc gcc agc acc ttg 144
Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
 35 40 45

tat gga att atg ttt gat gca ggg agc act gga act cga att cat gtt 192
Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
 50 55 60

tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta gaa ggg Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly 65 70 75 80	240
gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta gat caa Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln 85 90 95	288
cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg gcc aaa Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys 100 105 110	336
gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc cta aag Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys 115 120 125	384
gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag gct ctg Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu 130 135 140	432
ctc ttt gag gta aag gag atc ttc agg aag tca cct ttc ctg gta cca Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro 145 150 155 160	480
aag ggc agt gtt agc atc atg gat gga tcc gac gaa ggc ata tta gct Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala 165 170 175	528
tgg gtt act gtg aat ttt ctg aca ggt cag ctg cat ggc cac aga cag Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln 180 185 190	576
gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa atc acg Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr 195 200 205	624
ttc ctg ccc cag ttt gag aaa act ctg gaa caa act cct agg ggc tac Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr 210 215 220	672
ctc act tcc ttt gag atg ttt aac agc act tat aag ctc tat aca cat Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His 225 230 235 240	720
agt tac ctg gga ttt gga ttg aaa gct gca aga cta gca acc ctg gga Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly 245 250 255	768
gcc ctg gag aca gaa ggg act gat ggg cac act ttc cggttgt Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys 260 265 270	816
tta ccg aga tgg ttg gaa gca gag tgg atc ttt ggg ggt gtg aaa tac Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr 275 280 285	864
cag tat ggt ggc aac caa gaa ggg gag gtg ggc ttt gag ccc tgc tat Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr 290 295 300	912

gcc gaa gtg ctg agg gtg gta cga gga aaa ctt cac cag cca gag gag Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu 305 310 315 320	960
gtc cag aga ggt tcc ttc tat gct ttc tct tac tat tat gac cga gct Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala 325 330 335	1008
gtt gac aca gac atg att gat tat gaa aag ggg ggt att tta aaa gtt Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val 340 345 350 .	1056
gaa gat ttt gaa aga aaa gcc agg gaa gtg tgt gat aac ttg gaa aac Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn 355 360 365	1104
tcc acc tca ggc agt cct ttc ctg tgc atg gat ctc agc tac atc aca Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr 370 375 380	1152
gcc ctg tta aag gat ggc ttt ggc ttt gca gac agc aca gtc tta cag Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln 385 390 395 400	1200
ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg ggg gcc Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala 405 410 415	1248
acc ttt cac ctg ttg cag tct ctg ggc atc tcc cat tga Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His 420 425	1287

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35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
50 55 60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
65 70 75 80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
85 90 95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
100 105 110

Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
115 120 125

Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
130 135 140

Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
145 150 155 160

Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
165 170 175

Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
180 185 190

Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
195 200 205

Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
210 215 220

Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
225 230 235 240

Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
245 250 255

Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
260 265 270

Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
275 280 285

Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
290 295 300

Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
305 310 315 320

Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
325 330 335

Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
340 345 350

Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
355 360 365

Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
370 375 380

Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385 390 395 400

Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
405 410 415

Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
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gtt tgc agc gct gtc tcc cac agg aac cag cag act tgg ttt gag ggt 96
Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
20 25 30

atc ttc ctg tct tcc atg tgc ccc atc aat gtc agc gcc agc acc ttg 144
Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
35 40 45

tat gga att atg ttt gat gca ggg agc act gga act cga att cat gtt 192
Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
50 55 60

tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta gaa ggg 240
Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
65 70 75 80

gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta gat caa 288
Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
85 90 95

cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg gcc aaa 336
Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
100 105 110

gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc cta aag 384
Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
115 120 125

gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag gct ctg 432
Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
130 135 140

ctc ttt gag gta aag gag atc ttc agg aag tca cct ttc ctg gta cca 480
Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
145 150 155 160

aag ggc agt gtt agc atc atg act gga caa gac gaa ggc ata ttc gct 528
Lys Gly Ser Val Ser Ile Met Thr Gly Gln Asp Glu Gly Ile Phe Ala
165 170 175

tgg gtt act gtg aat ttt ctg aca ggt cag ctg cat ggc cac aga cag 576
Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
180 185 190

gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa atc acg 624
Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
195 200 205

ttc ctg ccc cag ttt gag aaa act ctg gaa caa act cct agg ggc tac 672
Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
210 215 220

ctc act tcc ttt gag atg ttt aac agc act tat aag ctc tat aca cat 720

Leu	Thr	Ser	Phe	Glu	Met	Phe	Asn	Ser	Thr	Tyr	Lys	Leu	Tyr	Thr	His
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Ser	Tyr	Leu	Gly	Phe	Gly	Leu	Lys	Ala	Ala	Arg	Leu	Ala	Thr	Leu	Gly
				245					250			255			
gcc	ctg	gag	aca	gaa	ggg	act	gat	ggg	cac	act	ttc	cg	agt	gcc	tgt
Ala	Leu	Glu	Thr	Glu	Gly	Thr	Asp	Gly	His	Thr	Phe	Arg	Ser	Ala	Cys
				260				265			270				
tta	ccg	aga	tgg	ttg	gaa	gca	gag	tgg	atc	ttt	ggg	ggt	gtg	aaa	tac
Leu	Pro	Arg	Trp	Leu	Glu	Ala	Glu	Trp	Ile	Phe	Gly	Gly	Val	Lys	Tyr
				275				280			285				
cag	tat	ggt	ggc	aac	caa	gaa	ggg	gag	gtg	ggc	ttt	gag	ccc	tgc	tat
Gln	Tyr	Gly	Gly	Asn	Gln	Glu	Gly	Glu	Val	Gly	Phe	Glu	Pro	Cys	Tyr
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gcc	gaa	gtg	ctg	agg	gtg	gta	cga	gga	aaa	ctt	cac	cag	cca	gag	gag
Ala	Glu	Val	Leu	Arg	Val	Val	Arg	Gly	Lys	Leu	His	Gln	Pro	Glu	Glu
				305			310			315			320		
gtc	cag	aga	ggt	tcc	ttc	tat	gct	ttc	tct	tac	tat	tat	gac	cga	gct
Val	Gln	Arg	Gly	Ser	Phe	Tyr	Ala	Phe	Ser	Tyr	Tyr	Tyr	Asp	Arg	Ala
				325			330			335					
gtt	gac	aca	gac	atg	att	gat	tat	gaa	aag	ggg	ggt	att	tta	aaa	gtt
Val	Asp	Thr	Asp	Met	Ile	Asp	Tyr	Glu	Lys	Gly	Gly	Ile	Leu	Lys	Val
				340			345			350					
gaa	gat	ttt	gaa	aga	aaa	gcc	agg	gaa	gtg	tgt	gat	aac	ttg	gaa	aac
Glu	Asp	Phe	Glu	Arg	Lys	Ala	Arg	Glu	Val	Cys	Asp	Asn	Leu	Glu	Asn
				355			360			365					
tcc	acc	tca	ggc	agt	cct	ttc	ctg	tgc	atg	gat	ctc	agc	tac	atc	aca
Phe	Thr	Ser	Gly	Ser	Pro	Phe	Leu	Cys	Met	Asp	Leu	Ser	Tyr	Ile	Thr
				370			375			380					
gcc	ctg	tta	aag	gat	ggc	ttt	gca	gac	agc	aca	gtc	tta	cag		1200
Ala	Leu	Leu	Lys	Asp	Gly	Phe	Gly	Phe	Ala	Asp	Ser	Thr	Val	Leu	Gln
				385			390			395			400		
ctc	aca	aag	aaa	gtg	aac	aac	ata	gag	acg	ggc	tgg	gcc	ttg	ggg	gcc
Leu	Thr	Lys	Lys	Val	Asn	Asn	Ile	Glu	Thr	Gly	Trp	Ala	Leu	Gly	Ala
				405			410			415					
acc	ttt	cac	cta	ttg	cag	tct	ctg	ggc	atc	tcc	cat	tga			1287
Thr	Phe	His	Leu	Leu	Gln	Ser	Leu	Gly	Ile	Ser	His				
				420			425								

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<212> PRT
<213> Homo sapiens

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20

25

30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
50 55 60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
65 70 75 80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
85 90 95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
100 105 110

Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
115 120 125

Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
130 135 140

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Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
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Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
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Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
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Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
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Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
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Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
355 360 365

Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
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Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
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Val Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp
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Ser Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg
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Ile His Val Tyr Thr Phe Val Gln Lys Met Pro
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aggaggtcca gagaggttcc ttctatgctt tctcttacta ttatgaccga gctgttgaca 1260
cagacatgat tgattatgaa aaggggggta tttaaaaagt tgaagatTTT gaaagaaaag 1320
ccagggaaat gtgtgataac ttggaaaaact tcacccctcagg cagtccttcc ctgtgcattgg 1380
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caggtgtgac ctctggcagc aaaaaaaaaa aaaaaaaaaa a 1601

<210> 25

<211> 405

<212> PRT

<213> Homo sapiens

<400> 25

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
20 25 30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
50 55 60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
65 70 75 80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
85 90 95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
100 105 110

Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
115 120 125

Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
130 135 140

Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
145 150 155 160

Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
165 170 175

Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
180 185 190

Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
195 200 205

Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
210 215 220

Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
225 230 235 240

Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
245 250 255

Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
260 265 270

Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
275 280 285

Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
290 295 300

Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
305 310 315 320

Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
325 330 335

Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
340 345 350

Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
355 360 365

Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
370 375 380

Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385 390 395 400

Ala Ala Val Leu Arg
405

<210> 26

<211> 2762

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (148)..(1599)

<400> 26

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gcgcggtgca tggaatgggc tatgtga atg aaa aaa ggt atc cgt tat gaa act 174
Met Lys Lys Gly Ile Arg Tyr Glu Thr
1 5

tcc aga aaa acg agc tac att ttt cag cag ccg cag cac ggt cct tgg 222
Ser Arg Lys Thr Ser Tyr Ile Phe Gln Gln Pro Gln His Gly Pro Trp
10 15 20 25

caa aca agg atg aga aaa ata tcc aac cac ggg agc ctg cggt gtg gcg 270
Gln Thr Arg Met Arg Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala
30 35 40

aag gtg gca tac ccc ctg ggg ctg tgt gty ggc gtc ttc atc tat gtt 318
Lys Val Ala Tyr Pro Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val
45 50 55

gcc tac atc aag tgg cac cg^g gcc acc g^c c^c a^g g^c ttc ttc agc 366
Ala Tyr Ile Lys Trp His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser
60 65 70

atc acc agg gca gcc cc^g ggg g^c c^g tgg ggt c^a g^a g^c c^a c^a agc 414
Ile Thr Arg Ala Ala Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser
75 80 85

ccc ctg ggg aca gct gca gac ggg cac gag gtc ttc tac ggg atc atg 462
Pro Leu Gly Thr Ala Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met
90 95 100 105

ttt gat gca gga agc act ggc acc cga gta cac gtc ttc cag ttc acc 510
Phe Asp Ala Gly Ser Thr Gly Thr Arg Val His Val Phe Gln Phe Thr
110 115 120

cgg ccc ccc aga gaa act ccc acg tta acc cac gaa acc ttc aaa gca 558
Arg Pro Pro Arg Glu Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala
125 130 135

gtg aag cca ggt ctt tct gcc tat gct gat gat gtt gaa aag agc gct 606
Val Lys Pro Gly Leu Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala
140 145 150

cag gga atc cg^g gaa cta ctg gat gtt gct aaa cag gac att cc^g ttc 654
Gln Gly Ile Arg Glu Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe
155 160 165

gac ttc tgg aag gcc acc cct ctg gtc ctc aag gcc aca gct ggc tta 702
Asp Phe Trp Lys Ala Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu
170 175 180 185

cgc ctg tta cct gga gaa aag gcc cag aag tta ctg cag aag gtg aaa 750
Arg Leu Leu Pro Gly Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys
190 195 200

gaa gta ttt aaa gca tcg cct ttc ctt gta ggg gat gac tgt gtt tcc 798
Glu Val Phe Lys Ala Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser
205 210 215

atc atg aac gga aca gat gaa ggc gtt tcg gc^g tgg atc acc atc aac 846
Ile Met Asn Gly Thr Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn
220 225 230

t^c t^c a^c g^g c^a g^c t^t g^a a^a a^c t^c c^a g^g a^g c^g a^g c^g g^g c^a t^g 894
Phe Leu Thr Gly Ser Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met
235 240 245

ctg gac ttg ggc gga gga tcc act cag atc gcc ttc ctg cca cgc gtg 942
Leu Asp Leu Gly Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val
250 255 260 265

gag ggc acc ctg cag gcc tcc cca ccc ggc tac ctg acg gca ctg cgg 990
Glu Gly Thr Leu Gln Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg
270 275 280

- 26 -

atg ttt aac agg acc tac aag ctc tat tcc tac agc tac ctc ggg ctc	1038
Met Phe Asn Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu	
285 290 295	
ggg ctg atg tcg gca cgc ctg gcg atc ctg ggc ggc gtg gag ggg cag	1086
Gly Leu Met Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln	
300 305 310	
cct gct aag gat gga aag gag ttg gtc agc cct tgc ttg tct ccc agt	1134
Pro Ala Lys Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser	
315 320 325	
ttc aaa gga gag tgg gaa cac gca gaa gtc acg tac agg gtt tca ggg	1182
Phe Lys Gly Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly	
330 335 340 345	
cag aaa gca gcg gca agc ctg cac gag ctg tgt gct gcc aga gtg tca	1230
Gln Lys Ala Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser	
350 355 360	
gag gtc ctt caa aac aga gtg cac agg acg gag gaa gtg aag cat gtg	1278
Glu Val Leu Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val	
365 370 375	
gac ttc tat gct ttc tcc tac tat tac gac ctt gca gct ggt gtg ggc	1326
Asp Phe Tyr Ala Phe Ser Tyr Tyr Asp Leu Ala Ala Gly Val Gly	
380 385 390	
ctc ata gat gcg gag aag gga ggc agc ctg gtg gtg ggg gac ttc gag	1374
Leu Ile Asp Ala Glu Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu	
395 400 405	
atc gca gcc aag tac gtg tgt cgg acc ctg gag aca cag ccg cag agc	1422
Ile Ala Ala Lys Tyr Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser	
410 415 420 425	
agc ccc ttc tca tgc atg gac ctc acc tac gtc agc ctg cta ctc cag	1470
Ser Pro Phe Ser Cys Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln	
430 435 440	
gag ttc ggc ttt ccc agg agc aaa gtg ctg aag ctc act cgg aaa att	1518
Glu Phe Gly Phe Pro Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile	
445 450 455	
gac aat gtt gag acc agc tgg gct ctg ggg gcc att ttt cat tac atc	1566
Asp Asn Val Glu Thr Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile	
460 465 470	
gac tcc ctg aac aga cag aag agt cca gcc tca tagtgccga gccatccctg	1619
Asp Ser Leu Asn Arg Gln Lys Ser Pro Ala Ser	
475 480	
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ctgaggagcc acagcacagg ccgtgctggc actttctgca cactggctct gggacttgca	1739
gaaggcctgg tgctgccctg gcatcagcct cttccagtca catctggcca gagggctgtc	1799
tggacctggg ccctgctcaa tgccacctgt ctgcctgggc tccaaagtggg caggaccagg	1859
acagaaccac aggcacacac tgagggggca gtgtggctcc ctgcctgtcc catccccatg	1919

ccccgtccgc ggggctgtgg ctgctgctgt gcatgtccct gcgatggag tcttgtctcc 1979
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aaa 2762

<210> 27
<211> 484
<212> PRT
<213> Homo sapiens

<400> 27
Met Lys Lys Gly Ile Arg Tyr Glu Thr Ser Arg Lys Thr Ser Tyr Ile
1 5 10 15

Phe Gln Gln Pro Gln His Gly Pro Trp Gln Thr Arg Met Arg Lys Ile
20 25 30

Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro Leu Gly
35 40 45

Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp His Arg
50 55 60

Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala Pro Gly
65 70 75 80

Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala Ala Asp
85 90 95

Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly
100 105 110

Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu Thr Pro
115 120 125

Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu Ser Ala

130	135	140
Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu Leu Leu		
145	150	155
Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala Thr Pro		
165	170	175
Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly Glu Lys		
180	185	190
Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala Ser Pro		
195	200	205
Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr Asp Glu		
210	215	220
Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser Leu Lys		
225	230	235
Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly Ser		
245	250	255
Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln Ala Ser		
260	265	270
Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr Tyr Lys		
275	280	285
Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala Arg Leu		
290	295	300
Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly Lys Glu		
305	310	315
Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp Glu His		
325	330	335
Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala Ser Leu		
340	345	350
His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn Arg Val		
355	360	365
His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe Ser Tyr		
370	375	380
Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu Lys Gly		
385	390	395
Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr Val Cys		
405	410	415
Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys Met Asp		
420	425	430
Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro Arg Ser		
435	440	445
Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr Ser Trp		
450	455	460

Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg Gln Lys
465 470 475 480

Ser Pro Ala Ser

<210> 28

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 28

cgtatccgc gggtgaggc cggggtg

27

<210> 29

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 29

cttctgcaag tcccagagcc agtgtgc

27

<210> 30

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 30

ggagcccaa a gacccggctg c

21

<210> 31

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 31

tgaagtacg tccaggacag g

21

<210> 32

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 32
cggaattcaa cataaaaaaa ggttatccgt tatgaa 36

<210> 33
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 33
tgtctagatg aggctggact cttctg 26

<210> 34
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide primer

<400> 34
atcctggact tgagcctaga g 21

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide primer

<400> 35
ctgatattga tgggtcttgg g 21

<210> 36
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide primer

<400> 36
ggatggaaag gagttggta g 21

<210> 37
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

- 31 -

oligonucleotide primer

<400> 37

gtccacatgc ttcacttcct c

21